

STIC-Biotech/ChemLib

78784

From: Helmer, Georgia
Sent: Friday, October 25, 2002 5:05 PM
To: STIC-Biotech/ChemLib
Subject: 09/805,550

would you please do a sequence search in case 09/805,550 on

SEQ ID 2 and 4 - polypeptides

SEQ ID 1 and 3 - polynucleotides,\

and an oligo search on # 1 and 3.

Thanks in advance

Georgia L. Helmer Ph.D.
Patent Examiner
Crystal Mall 1, 9D14
AU 1638
703-308-7023
Georgia.Helmer@USPTO.gov
mailbox 9e12

mc. excision report

11/02
✓ gth
no pending

2 - 405

4 368

20 cont	80
4.9%	385
5.4%	348

70%

SID2 OK
4 OK
70% OK
20 mar OK
gth

the data is fine

Point of Contact:
Barb O'Brien
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB
Phone: _____
Location: _____
Date Picked Up: 11-1
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

completed 11-4-02

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

RECEIVED
JAN 10 1968
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HONOLULU, HAWAII

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OM protein - protein search, using sw model

Run on: November 3, 2002, 23:27:20 ; Search time 49.7736 Seconds
(without alignments)
1084.239 Million cell updates/sec

Title: US-09-805-550-2

Perfect score: 2036
Sequence: 1 MRLNVTKLKGTNFEIEASPD.....ELTANYLLDHGHEPDDQ00 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2036	100.0	405	21	AAV71458
2	1199.5	58.9	378	21	AAG19974
3	1199.5	58.9	378	21	AAAG5204
4	1095	53.8	335	21	AAAG1975
5	1095	53.8	335	21	AAAG5205
6	981	48.2	307	21	AAAG1976
7	981	48.2	307	21	AAAG5206
8	945.5	46.4	371	21	AAAG17377
9	913	44.8	368	21	AAAG4341
10	900.5	44.2	368	21	AAV71459

11	881.5	43.3	348	21	AAAG17378	Arabidopsis thalia
12	850	41.7	345	21	AAAG44342	Arabidopsis thalia
13	754.5	37.1	299	21	AAAG17379	Arabidopsis thalia
14	732	36.0	257	21	AAAG36529	Arabidopsis thalia
15	725	35.6	296	21	AAAG4343	Arabidopsis thalia
16	634	31.1	409	19	AAV75700	Vpr protein bindin
17	634	31.1	409	19	AAV68186	Vpr protein bindin
18	628.5	30.9	214	21	AAAG36530	Arabidopsis thalia
19	623.5	30.6	463	23	ABBS7171	Mouse ischaemic co
20	573	28.1	363	18	AAV23658	E6AP-binding prote
21	573	28.1	363	19	AAV75699	Vpr protein bindin
22	573	28.1	363	19	AAV68185	Vpr protein bindin
23	572.5	28.1	379	21	AAV58841	Breast and ovarian
24	548	26.9	346	18	AAV21730	Nuclear mitotic ap
25	514.5	25.3	186	21	AAAG36531	Arabidopsis thalia
26	481	23.6	414	22	ABBS58584	Drosophila melanog
27	347	17.0	179	19	AAV75843	Vpr protein bindin
28	347	17.0	179	19	AAV68187	Vpr binding protel
29	324	15.9	174	19	AAV75850	Protein sequence o
30	324	15.9	174	19	AAV68194	Protein sequence o
31	318	15.6	117	23	ABP34618	Drosophila melanog
32	317	15.6	290	22	ABBS72011	Human ORF3591 prot
33	307	15.1	136	21	AAAG3942	Arabidopsis thalia
34	289	14.2	150	19	AAV75849	Protein sequence o
35	289	14.2	150	19	AAV68193	Protein sequence o
36	229	11.2	112	19	AAV75848	Protein sequence o
37	229	11.2	112	19	AAV68192	Protein sequence o
38	211	10.4	536	21	AAAG30040	Arabidopsis thalia
39	211	10.4	577	21	AAAG30039	Arabidopsis thalia
40	201	9.9	504	22	ABG16557	Novel human diagno
41	197.5	9.7	596	22	AAAG4210	Murine HSP47 inter
42	197	9.7	589	22	AAAG4008	Human stomach canc
43	197	9.7	589	22	AAV94311	Human protein sequ
44	197	9.7	589	22	AAV95205	Human protein sequ
45	197	9.7	589	22	AAV62194	Human SAP2 amino a

ALIGNMENTS

RESULT 1
ID AAV71458 standard; Protein: 405 AA.
XX
AC AAV71458;
XX
04-OCT-2000 (first entry)
XX
DE Maize Rad23 protein #1.
XX
XX Rad23; maize; ATCC No: PTA-530; recombinant expression cassette; wheat;
KW transgenic plant; soybean; sunflower; sorghum; canola; modulator.
XX
OS Zea mays.
XX
PN WO200031268-A1.
XX
PD 02-JUN-2000.
XX
PE 12-OCT-1999; 99WO-US24129.
XX
PR 23-NOV-1998; 98US-0109728.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Mahajan PB, Tagliani L;
XX
DR WPI: 2000-400078/34.
XX
PT N-PSDB: AAD01230.
PT Isolated nucleic acid encoding maize RAD23 protein is used to modulate
the levels of polypeptides in plant or in assays for identifying
compounds that bind to and/or increase/decrease enzymatic activity of

PT catalytically active polypeptides -
XX Clam 11b; Page 75-76; 82pp; English.
XX The present sequence is the maize Rad23 protein #1. It is isolated from
CC V5 root tissue of a Zea mays cell line B73, infested with corn root
CC worm. The cDNA sequence is deposited under the ATCC No: PTA-530. Maize
CC Rad23 DNA sequence operably linked to a promoter can be used to construct
CC a recombinant expression cassette. This expression cassette can be used
CC to generate a dicot or monocot transgenic plant e.g., maize, soybean,
CC sunflower, sorghum, canola, wheat, etc.. It can also be used to modulate
CC the levels of Rad23 polypeptide expression in a plant or in assays to
CC identify compounds, that bind to and/or modulate the enzymatic activity
CC of catalytically active polypeptides.
XX
XX Sequence 405 AA;
SQ
Query Match 100.0%; Score 2036; DB 21; Length 405;
Best Local Similarity 100.0%; Pred. No. 6.1e-138;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLNWKTKLGTNFEIEASPDASVADVKRIETTGOSTYRADQOMLIYQKILKDETTLE 60
OY 61 SNGVAFENSLVYMLSKAKSSGASATTTAKAPATLQPAAYAPAAVARTPTQAPVAT 120
DB 61 SNGVAFENSLVYMLSKAKSSGASATTTAKAPATLQPAAYAPAAVARTPTQAPVAT 120
OY 121 AETAPPVQPOAAPATVATDADVYSQASNLVFGNMLEQTIOILMGSGTWERDTY 180
DB 121 AETAPPVQPOAAPATVATDADVYSQASNLVFGNMLEQTIOILMGSGTWERDTY 180
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DB 181 VRLAARAYNNPRAIDYLYSGIPEVNEAQPVARAPAAQGTQQAASPAQPAVALPVQPS 240
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DB 241 PASAGPNNAPLPLFPGQVSGSGNGVYPGAGSALDALRQLPQOALLQYVQANPQITQ 300
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DB 301 PMLQELGKONPQILRLIOENQAEFLRLVNESPEGGPGGNIQLAAVPTQLVTPPEERE 360
OY 361 AIORLGEMGFNRELVEVFFACNKDELTANYLLDHGHEFDQOO 405
DB 361 AIORLGEMGFNRELVEVFFACNKDELTANYLLDHGHEFDQOO 405
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AAG19974
ID AAG19974 standard; Protein; 378 AA.
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XX AAG19974;
AC
XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 21981.
DE
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
PR

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Query Match 58 98; Score 1199.5; DB 21; Length 378;
 Best Local Similarity 62.98; Pred. No. 5.2e-78;

Matches 256; Conservative 43; Mismatches 75; Indels 33; Gaps 9;

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 Db 1 MKIFVKTLSSGNFEIEVKPAKVSADVKALETYKG-AEYPAKGMILHOGKVLNDETTL 59
 QY 61 SNGVAENSEFLVIMLSKAKASSGASSTAT-TAKAPATLAQAPAPAPASVARTPTQA 116
 Db 60 ENNVVENSFIYIMLSKTKASPSGASTASAPASATQPTVATPOVS-APTASV----- 111
 QY 117 PVATAETAPPEVQPOAAPATVAATDDADVYSOASNLVFNENNETTOITQOITLMDGGTWE 176
 Db 112 FVPTSGTA-----TAAAPA--TAASVOTDYVGOAASNLVAGTTLESTVQOITLMDGGSSWD 164
 QY 177 RDTVVRALRAAYNNPERAIDLYSGIPENVEAQPVARAPAGOOTNOOASPAQPAVALP 236
 Db 165 RDTVVRALRAAFNNPERAVERVELYSGIPQAQELIPYQAQAPATGBOANPLAQPOQAAA--- 221
 QY 237 VQSPASAGPNANPLNLEPQGVPSGSGNPVYPGAGSGALDALRQLPQFALLQYQANP 296
 Db 222 --PAAATGPNANPLNLEPQGMPAADA-----GAGAGNIDFLRNSOQFOALRAVQANP 273
 QY 297 QILQPMIOELGKONPOLRLQENQAEFLRLVNSPEGGPGCNILIGQAAAVPQTLVTP 356
 Db 274 QILQPMIOELGKONPOLRLQEHQADFLRLINEPVEGEE--NWMEOLEAMPQAVVTP 331
 QY 357 EEREAIQRLGEMGFNRELVLVEFFACNDEDELTANYLLDHDHERPDQ 403
 Db 332 EEREAIERLBGMGFDRANVLVEFFACNKNBELANYLLDHNHHEREDQ 378

DT	18-OCT-2000	(first entry)
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 56723.	
DE	Protein identification; signal transduction pathway; metabolic pathway;	
XX	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
OS	Arabidopsis thaliana.	
XX	EPI033405-A2.	
PN	06-SEP-2000.	
XX		
PD	25-FEB-2000; 2000EP-0301439.	
PF		
XX	25-FEB-1999; 99US-0121825.	
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PR	28-MAY-1999; 99US-0136782.	
PR	01-JUN-1999; 99US-0137222.	
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PR	07-JUN-1999; 99US-0137724.	
PR	08-JUN-1999; 99US-0138094.	
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Oy	177	RDTVVRLRAAYNNPERIDLYSGIPENVPAOVAPARAAGOOTNOQAASPAOPAYALP	236		
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Dd	165	RDTVVRLRAAFENNPERAVETLISGITPAQAEIIPPVADAPATGEQANPLAQOGAAA---	221		
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Dd	274	QILQMLOELGKONPOLYRLRIOEHADPLRLLINEVEE--NVMEQLAEAMPQAVTVTP	331
Oy	357	EEREAIQRLEGGKFNRELVLVEFFACNKDEBLTANYLLDHGHEFDQ	403
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XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 21982.	
XX	KW	Protein identification: signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.	
XX	OS	Arabidopsis thaliana.	
XX	PN	EP1033405-AZ.	
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DT 18-OCT-2000 (first entry)
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KM Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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Best Local Similarity 62.7%; Pred. No. 1.8e-62;
Matches 210; Conservative 34; Mismatches 59; Indels 32; Gaps 8;

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DB 49 -TAAPAA--TAAVQTVDYGOASNLVAGTTLESTVOIILDMGGGSDWRDVTVALRAAF 105
QY 189 NNPERAIDLYSGIPENVEADPVARAPAGQOTNOCAASPOPAVALPVOPSPASAPNA 248
DB 106 NNPERAVEIYLSGIPAAAEIPVAPATGEOANPLAQPOQAAA-----PAATGSPNA 160
QY 249 NPLNLFPQGVPSGSGSNGGVDPGAGSGALDLRLQPLPQALQLQVQANPQIILQMLQELGK 308
DB 161 NPLNLFPQGMFAADA-----GAGAGMLDLFRNSQOFOALRAMVOANPQIILQMLQELGK 214
QY 309 ONPQIILRIENQAEFLRLVNESPEGGNIILOLAAYPQTLTPPEREATORLEGM 368
DB 215 ONPQVLRILIOHQADFLRLINEPEGEE--NVMQLENAHQAVTVPEREATERLEGM 272
QY 369 GFNNRELVLEVFACNKKDELTANYLLDGHFEFDDQ 403
DB 273 GFDRNAVLEVFACNKNDELAANYLLDHMEFEEDQ 307
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Qy	294	ANPQILOPMLOELKONFOILRLIOENOAEPFLRVNSPEGGPG--GNILGOLAAAVPQTL		352
Db	262	SNFOILQPMLOELKONFOILRLIOENOAEPFLRVNPEYSGSDGGMFQPGQENPHAI		321
Qy	353	TVTPPEAREALIQLEGMGFNRELVEFPACNKDELTANTYLLDHGFDD		402
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KW		hybridisation assay; genetic mapping; gene expression control; promoter;		
KW		termination sequence.		
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OS		Arabidopsis thaliana.		
XX				
PN		EP1033405-A2.		
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PD		06-SEP-2000.		
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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Query Match

44.8%; Score 913; DB 21; Length 368;

Best Local Similarity 47.5%; Pred. No. 1,7e-57; Matches 194; Conservative 64; Mismatches 104; Indels 46; Gaps 7;

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 1 MKLVNKTGKNEIEASPDASVADYKRIIETGOSTYRADQOMLIYQKILKDETTLE 60
 1 MKLVNKTGKNEIEASPDASVADYKRIIETGOSTYRADQOMLIYQKILKDETTLE 60
 1 MKLVNKTGKNEIEASPDASVADYKRIIETGOSTYRADQOMLIYQKILKDETTLE 60

QY 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 120
 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 120
 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 120
 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 120

QY 121 AETAPPSVQQAAPATVA-----ATDDADYSOAASNLVFGNNLEOTIOIIMGGGTW 175
 121 AETAPPSVQQAAPATVA-----ATDDADYSOAASNLVFGNNLEOTIOIIMGGGTW 175
 121 AETAPPSVQQAAPATVA-----ATDDADYSOAASNLVFGNNLEOTIOIIMGGGTW 175
 121 AETAPPSVQQAAPATVA-----ATDDADYSOAASNLVFGNNLEOTIOIIMGGGTW 175

QY 102 TLAPSTOSIAVPASSTVQEQPTAQOSTYGOASTVSGSTIEQVQOIMEMGGSW 161
 102 TLAPSTOSIAVPASSTVQEQPTAQOSTYGOASTVSGSTIEQVQOIMEMGGSW 161
 102 TLAPSTOSIAVPASSTVQEQPTAQOSTYGOASTVSGSTIEQVQOIMEMGGSW 161
 102 TLAPSTOSIAVPASSTVQEQPTAQOSTYGOASTVSGSTIEQVQOIMEMGGSW 161

QY 176 ERDTPVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 235
 176 ERDTPVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 235
 176 ERDTPVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 235
 176 ERDTPVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 235

QY 162 DKETVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 211
 162 DKETVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 211
 162 DKETVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 211
 162 DKETVRAALAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPVAL 211

QY 236 PVQSPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 295
 236 PVQSPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 295
 236 PVQSPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 295
 236 PVQSPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 295

QY 212 -----PPSGSPNSPLDLFPQEAASDA-----GCDLGLTEFLRGNDQFQQLRSMVNSN 260
 212 -----PPSGSPNSPLDLFPQEAASDA-----GCDLGLTEFLRGNDQFQQLRSMVNSN 260
 212 -----PPSGSPNSPLDLFPQEAASDA-----GCDLGLTEFLRGNDQFQQLRSMVNSN 260
 212 -----PPSGSPNSPLDLFPQEAASDA-----GCDLGLTEFLRGNDQFQQLRSMVNSN 260

QY 296 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 354
 296 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 354
 296 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 354
 296 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 354

QY 261 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 320
 261 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 320
 261 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 320
 261 PQLQPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 320

QY 355 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 402
 355 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 402
 355 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 402
 355 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 402

QY 321 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 368
 321 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 368
 321 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 368
 321 TPPEERAIORLEGMGFNRELVEVFACNKEDELTANYLLDHGHEFD 368

RESULT 10
 AAY71459
 ID AAY71459 standard; Protein; 368 AA.
 AC AAY71459;
 XX
 DT 04-OCT-2000 (first entry)
 XX
 DE Maize Rad23 protein #2.
 XX
 KM Rad23; maize; ATCC No: PTA-531; recombinant expression cassette; wheat;
 KM transgenic plant; soybean; sunflower; sorghum; canola; modulator.
 XX
 OS Zea mays.
 OS
 PN W0200031268-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 12-OCT-1999; 99WO-US24129.
 XX
 PR 23-NOV-1998; 98US-0109728.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Mahajan PB, Tagliani L;
 XX
 DR WPI: 2000-400078/34.
 DR N-PSDB: AAD01231.
 XX
 XX Isolated nucleic acid encoding maize RAD23 protein is used to modulate
 PT the levels of polypeptides in plant or in assays for identifying
 PT compounds that bind to and/or increase/decrease enzymatic activity of
 PT catalytically active polypeptides -
 XX
 PS Claim 11b; Page 78-79; 82pp; English.
 XX
 CC The present sequence is the maize Rad23 protein #2. It is isolated from
 CC a Zea mays cell line, B73 callus tissue regenerated five days after
 CC transfer of the callus from medium containing auxin to a medium devoid
 CC of exogenous auxin. The cDNA is deposited under the ATCC No: PTA-531.

CC Maize Rad23 DNA sequence operably linked to a promoter, can be used to
 CC construct a recombinant expression cassette. This expression cassette
 CC can be used to generate a dicot or monocot transgenic plant e.g., maize,
 CC soybean, sunflower, sorghum, canola, wheat, etc., It can also be used to
 CC modulate the levels of Rad23 polypeptide expression in a plant or in
 CC assays to identify compounds, that bind to and/or modulate the enzymatic
 CC activity of catalytically active polypeptides.

SQ Sequence 368 AA;
 Query Match 44.2%; Score 900.5; DB 21; Length 368;
 Best Local Similarity 49.0%; Pred. No. 1.4e-56;
 Matches 197; Conservative 53; Mismatches 117; Indels 35; Gaps 7;

QY 1 MKLVNKTGKNEIEASPDASVADYKRIIETGOSTYRADQOMLIYQKILKDETTLE 60
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 1 MKLVNKTGKNEIEASPDASVADYKRIIETGOSTYRADQOMLIYQKILKDETTLE 60
 1 MKLVNKTGKNEIEASPDASVADYKRIIETGOSTYRADQOMLIYQKILKDETTLE 60

QY 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 119
 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 119
 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 119
 61 SNGVAENSLYIMLSKAKASSGASTATTAKAPATTAQAPAPAPASVARTPTQAPVA 119

QY 61 ENKVNEDGFLVVMLSKGTSGTGTSSOHSNTPATQAP-----PLEAPQAP-QPVA 114
 61 ENKVNEDGFLVVMLSKGTSGTGTSSOHSNTPATQAP-----PLEAPQAP-QPVA 114
 61 ENKVNEDGFLVVMLSKGTSGTGTSSOHSNTPATQAP-----PLEAPQAP-QPVA 114
 61 ENKVNEDGFLVVMLSKGTSGTGTSSOHSNTPATQAP-----PLEAPQAP-QPVA 114

QY 120 TAETAPPSVQQAAPATVAATDDADYSSOASNLVFGNNLEOTIOIIMGGGTWERDT 179
 120 TAETAPPSVQQAAPATVAATDDADYSSOASNLVFGNNLEOTIOIIMGGGTWERDT 179
 120 TAETAPPSVQQAAPATVAATDDADYSSOASNLVFGNNLEOTIOIIMGGGTWERDT 179
 120 TAETAPPSVQQAAPATVAATDDADYSSOASNLVFGNNLEOTIOIIMGGGTWERDT 179

QY 115 PITTSQEPGLPAQAP-----NTHDNAASNLVSGRNVDITINQIMEMGGSWDKD 164
 115 PITTSQEPGLPAQAP-----NTHDNAASNLVSGRNVDITINQIMEMGGSWDKD 164
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QY 180 VVRLARAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPALPVQ 239
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QY 165 VQRLARAAVNNPERAIDLYSGIPENVEAOPVAPAPACQOTNOQASPAQAPALPVQ 213
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QY 240 SPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 299
 240 SPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 299
 240 SPASAGPAPNPLNLEPQVSPSGSGSNPGVPGAGSGALDALROLPOFALLQVQAN 299
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QY 214 -GLSGIPNTAPLDLFPQGAASNAG-----GAGGCPDPLFLNNPQFQAVREMYHTNPQIL 266
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 214 -GLSGIPNTAPLDLFPQGAASNAG-----GAGGCPDPLFLNNPQFQAVREMYHTNPQIL 266

QY 300 QPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 359
 300 QPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 359
 300 QPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 359
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QY 267 QPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 326
 267 QPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 326
 267 QPMLOELGKONPQILRLIENQAEFLRLYNESPEGGG-NILGQLAAVPTQILTY 326
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QY 360 EATQRLGEMGFNRELVEVFACNKEDELTANYLLDHGHEFD 401
 360 EATQRLGEMGFNRELVEVFACNKEDELTANYLLDHGHEFD 401
 360 EATQRLGEMGFNRELVEVFACNKEDELTANYLLDHGHEFD 401
 360 EATQRLGEMGFNRELVEVFACNKEDELTANYLLDHGHEFD 401

QY 327 EATQRLGEMGFNRELVEVFACNKEDELTANYLLDHGHEFD 368
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RESULT 11
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 ID AAG17378 standard; Protein; 348 AA.
 AC AAG17378;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 18373.
 XX
 KM Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX
 OS Arabidopsis thaliana.
 OS
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
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 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.

PR	08-APR-1999;	990S-0128714.
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PR	23-JUN-1999;	990S-0140354.
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PR	28-JUL-1999;	990S-0145919.
PR	28-JUL-1999;	990S-0145951.
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PR	02-AUG-1999;	990S-0146388.
PR	03-AUG-1999;	990S-0146389.
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PR	05-AUG-1999;	990S-0147199.
PR	05-AUG-1999;	990S-0147260.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 15-SEP-1999; 99US-0154018.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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